ABSTRACT:
By analyzing plant samples found at crime scenes, investigators can pull crucial pieces of information needed in their finding of criminals. In this study, we analyzed 20 species of weeds. Weeds usually are small plants which are more likely to be found on a criminal's clothing than large plants. Therefore, we demonstrated that the weed samples can be successfully identified through DNA barcoding techniques. The plants were previously collected from Brooklyn and Long Island, New York City (Sawyer, 2020). They were randomly selected bacterial plants that are less than one meter tall. Barcoding was carried out previously (Sawyer, 2020) using plantcocktail primers consisting of primers rbcLaF and rbcLaR (Cold Spring Harbor Laboratory DNA Learning Center (2014)). In this study, existing DNA sequences of plant samples were analyzed. A total 28 pairs of sequences were analyzed in this study.

INTRODUCTION:
In criminal investigations, the analysis of plant materials can aid investigators find crucial leads. There are thousands of different plants, which are common in NYC. In criminal investigations, the analysis of plant materials can aid investigators find crucial leads. For example, forensic investigators can compare the plant samples left behind at a crime scene with those on suspects to establish a connection. Thus, plant samples left at a crime scene can be useful evidence for investigations.

METHODS AND MATERIALS
Sample Preparation and Collection
The plants were previously collected from Brooklyn and Long Island, New York City (Sawyer, 2020). They were randomly selected bacterial plants that are less than one meter tall. Barcoding was carried out previously (Sawyer, 2020) using plantcocktail primers consisting of primers rbcLaF and rbcLaR (Cold Spring Harbor Laboratory DNA Learning Center (2014)). In this study, existing DNA sequences of plant samples were analyzed. A total 28 pairs of sequences were analyzed in this study.

RESULTS
Out of the 28 samples, we were able to identify 27 of them. One sample had insufficient data due to its poor quality of sequencing results. From the species identified, we selected the 20 small plants that can be considered as weeds. Figure 1 illustrates representative plant samples identified in this study. There were 7 samples of each of the species surveyed in this study. One sample had insufficient data due to its poor quality of sequencing results. All samples resulted in a bit score equal to or greater than 87. Bit score indicates the overall quality of the alignment. The higher the bit score value, the higher the alignment quality between the sequence in question and the known sequence in the database. Additionally, all results resulted in an E-value of 0. The lower the E-value, the higher the confidence in sequence comparison. Table 1 shows the phylogenetic relationship of the weeds surveyed in this study.

DISCUSSION
Through this study, we demonstrated that weeds found in NYC can be successfully identified using DNA barcoding techniques. The phylogenetic analysis demonstrates how we can identify certain plants in relation to others. By organizing the plant samples into a phylogenetic tree, we are able to categorize them by most related species. The analysis demonstrates how we can identify certain plants in relation to others. Therefore, this study demonstrates that identifying weed species can be successfully applied for the investigations of crimes.

REFERENCES

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